

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 31, 2005, 18:10:30 ; Search time 20 Seconds
(without alignments)
48.108 Million cell updates/sec

Title: US-10-083-768-5

Perfect score: 25

Sequence: 1 XXGXXXXXXW 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	68.0	72	2 H90603	hypothetical prote
2	17	68.0	132	2 C41855	hypothetical 14.2K
3	17	68.0	165	2 A83349	hypothetical prote
4	17	68.0	203	2 T50044	superoxide dismuta
5	17	68.0	239	2 T37065	hypothetical prote
6	17	68.0	251	2 A84019	NADPH-flavin oxido
7	17	68.0	272	2 T15820	hypothetical prote
8	17	68.0	297	2 E96002	probable sugar upt
9	17	68.0	308	2 B84311	hypothetical prote
10	17	68.0	406	2 A47696	acetamidase - Myco
11	17	68.0	408	2 D70549	hypothetical prote
12	17	68.0	408	2 H87193	probable FAD-link
13	17	68.0	433	2 C59222	hypothetical prote
14	17	68.0	492	2 T39591	hemolysin - Aetomo
15	17	68.0	523	2 T36677	probable secretory
16	17	68.0	547	2 A95861	hypothetical prote
17	17	68.0	579	2 T35240	probable secreted
18	17	68.0	624	2 S74222	alpha-galactosidas
19	17	68.0	735	2 AC0858	conserved hypotet
20	17	68.0	776	1 JQ2022	outer layer protei
21	17	68.0	776	1 JQ2023	outer layer protei
22	17	68.0	776	1 VPXRBU	outer layer protei
23	17	68.0	776	1 VPXR36	outer layer protei
24	17	68.0	776	1 VPXR36	outer layer protei
25	17	68.0	776	1 VPXR31	outer layer protei
26	17	68.0	776	1 VPXR31	outer layer protei
27	17	68.0	776	1 VPXR31	outer layer protei
28	17	68.0	776	2 A48480	outer capsid prote
29	17	68.0	776	2 S03611	outer layer protei

30	17	68.0	823	2 T02812	probable membrane
31	17	68.0	870	2 AB0570	outer membrane ush
32	17	68.0	1029	2 F96602	hypothetical prote
33	17	68.0	1156	2 S19306	parasporeal crystal
34	17	68.0	1275	1 S53636	ribulose-bisphosph
35	17	68.0	1546	2 G90603	lipoprotein (impor
36	17	68.0	1596	2 AG2501	hypothetical prote
37	17	68.0	1680	1 C5MS	complement C5 prec
38	17	68.0	2062	2 G96602	probable receptor
39	17	68.0	2204	1 RRNZNV	genome polyprotein
40	17	68.0	4563	1 LPHUB	apolipoprotein B-1
41	17	68.0	4660	2 T42737	gp330 protein prec
42	16	64.0	12	2 FQ0776	NADH2 dehydrogenas
43	16	64.0	60	2 AC2981	hypothetical prote
44	16	64.0	66	2 T35419	small hypothetical
45	16	64.0	70	2 A30518	Ig heavy chain V-A

ALIGNMENTS

RESULT 1

H90603

hypothetical protein MYPV_7360 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: H90603

R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galissou, F.; Moszer, I.;

Nucleic Acids Res. 29, 2145-2153, 2001

A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm

A;Reference number: A99512; MUID:21267165; PMID:11353084

A;Accession: H90603

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-72 <KUR>

A;Cross-references: UNIPROT:Q98PI6; GB:AL445566; PID:gl4090151; PIDN:CAC13909.1; GSPDB:G

A;Experimental source: strain UAB CTIP

C;Genetics:

A;Gene: MYPV_7360

A;Genetic code: SGC3

Query Match 68.0%; Score 17; DB 2; Length 72;
Best Local Similarity 28.6%; Pred. No. 8.6e+02;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy	3	GXXXXXW	9
Db	39	GAATSW	45

RESULT 2

C41855

hypothetical 14.2K beta-lactamase regulatory protein - Streptomyces cacaoi
C;Species: Streptomyces cacaoi
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: C41855

R;Urabe, H.; Ogawara, H.

J. Bacteriol. 174, 2834-2842, 1992

A;Title: Nucleotide sequence and transcriptional analysis of activator-regulator protein:

A;Reference number: A41855; MUID:92234939; PMID:1569015

A;Accession: C41855

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-132 <URA>

A;Cross-references: UNIPROT:P33654; GB:P00937; NID:g216997; PIDN:BAA00776.1; PID:g217001

A;Note: sequence extracted from NCBI backbone (NCBIN:97018, NCBI:97029)

C;Superfamily: Streptomyces cacaoi hypothetical 14.2K beta-lactamase regulatory protein

Query Match 68.0%; Score 17; DB 2; Length 132;
Best Local Similarity 28.6%; Pred. No. 1.4e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy	3	GXXXXXW	9
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Db      53 GSSASSW 59

RESULT 3
A83349
hypothetical protein PA2367 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: A83349
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83349
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-165 <STO>
A;Cross-references: UNIPROT:Q911B2; GB:AE004663; GB:AE004091; NID:g9948405; PIDN:AAG0575
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA2367

Query Match      68.0%; Score 17; DB 2; Length 165;
Best Local Similarity 28.6%; Pred. No. 1.7e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3 GXXXXXXW 9
Db      150 GTAATW 156

RESULT 4
T50044
superoxide dismutase (EC 1.15.1.1) (Mn) [similarity] - Haloarcula marismortui
C;Species: Haloarcula marismortui
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T50044
R;Joshi, P.B.; Dennis, P.P.
J. Bacteriol. 175, 1561-1571, 1993
A;Title: Characterization of paralogous and orthologous members of the superoxide dismut
A;Reference number: Z25029; MUID:93194779; PMID:8449865
A;Accession: T50044
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-203 <JOS>
A;Cross-references: UNIPROT:Q03302; EMBL:M97485; NID:g148741; PIDN:AAV73374.1; PID:g1487
C;Genetics:
A;Gene: sod
C;Superfamily: superoxide dismutase (Mn)
C;Keywords: manganese; metalloprotein; oxidoreductase

Query Match      68.0%; Score 17; DB 2; Length 203;
Best Local Similarity 28.6%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3 GXXXXXXW 9
Db      60 GSSAAW 66

RESULT 5
T37065
hypothetical protein SCJ21.16 - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37065
R;Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
A;Reference number: Z21620
A;Accession: T37065

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-272 <MAR>
A;Cross-references: UNIPROT:Q18776; EMBL:U41276; NID:g1086884; PID:g1086886; PIDN:AAA8246
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:C52B11.2
A;Introns: 12/1; 91/3; 190/3; 221/3

Query Match      68.0%; Score 17; DB 2; Length 272;
Best Local Similarity 28.6%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3 GXXXXXXW 9
Db      77 GSSSSW 83

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-239 <SEE>
A;Cross-references: UNIPROT:Q9S121; EMBL:AL109747; PIDN:CAB52362.1; GSPDB:GN00070; SCOREDI
C;Genetics:
A;Gene: SCOEDB:SCJ21.16

Query Match      68.0%; Score 17; DB 2; Length 239;
Best Local Similarity 28.6%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3 GXXXXXXW 9
Db      172 GASAAW 178

RESULT 6
A84019
NADPH-flavin oxidoreductase BH2953 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: A84019
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A84019
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-251 <STO>
A;Cross-references: UNIPROT:Q9K8Q0; GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BA0066;
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2953
C;Superfamily: NADPH-flavin oxidoreductase homolog

Query Match      68.0%; Score 17; DB 2; Length 251;
Best Local Similarity 28.6%; Pred. No. 2.4e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3 GXXXXXXW 9
Db      211 GATTTW 217

RESULT 7
T15820
hypothetical protein C52B11.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15820
R;Martin, J.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C52B11.
A;Reference number: Z18411
A;Accession: T15820
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-272 <MAR>
A;Cross-references: UNIPROT:Q18776; EMBL:U41276; NID:g1086884; PID:g1086886; PIDN:AAA8246
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:C52B11.2
A;Introns: 12/1; 91/3; 190/3; 221/3

Query Match      68.0%; Score 17; DB 2; Length 272;
Best Local Similarity 28.6%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3 GXXXXXXW 9
Db      77 GSSSSW 83

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RESULT 8
E96002
Probable sugar uptake ABC transporter permease protein Smb21459 [imported] - Sinorhizobium
C:Species: Sinorhizobium meliloti
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: E96002
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: E96002
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-297 <KUR>
A:Cross-references: UNIPROT:Q92U54; GB:AL591985; PIDN:CAC49685.1; PID:gl5141172; GSPDB:C
A:Experimental source: strain 1021, megaplasmid pSymb
R:Galibert, F.; Finan, T.M.; Long, S.R.; Fuhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: Smb21459
A:Genome: plasmid
C:Superfamily: inner membrane protein ugpA

Query Match 68.0%; Score 17; DB 2; Length 297;
Best Local Similarity 28.6%; Pred. No. 2.7e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GXXXXXX 9
Db 268 GAAASTW 274

RESULT 9
B84311
Hypothetical protein Vng1578h [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: B84311
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: B84311
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-308 <STO>
A:Cross-references: UNIPROT:Q9HPL3; GB:AE004437; NID:g10581062; PIDN:AAG19854.1; GSPDB:C
C:Genetics:
A:Gene: VNG1578H
C:Superfamily: cobalamin biosynthesis protein D

Query Match 68.0%; Score 17; DB 2; Length 308;
Best Local Similarity 28.6%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GXXXXXX 9
Db 172 GAAAAAW 178

RESULT 10

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A47696
Acetamidase - Mycobacterium smegmatis
C:Species: Mycobacterium smegmatis
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A47696
R:Manenthiralingam, E.; Draper, P.; Davis, E.O.; Colston, M.J.
J. Gen. Microbiol. 139, 575-583, 1993
A:Title: Cloning and sequencing of the gene which encodes the highly inducible acetamida
A:Reference number: A47696; MUID:93232774; PMID:8473863
A:Contents: NCTC 8159
A:Accession: A47696
A:Status: preliminary
A:Molecule type: DNA; protein
A:Residues: 1-406 <MAH>
A:Cross-references: UNIPROT:Q07838; GB:X57175; GB:S59037; NID:g312080; PIDN:CAA40462.1;
A:Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:129965, NCBIP:129966)

Query Match 68.0%; Score 17; DB 2; Length 406;
Best Local Similarity 28.6%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GXXXXXX 9
Db 370 GASAAASW 376

RESULT 11
D70549
Hypothetical protein Rv0561c - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: D70549
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: D70549
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-408 <COL>
A:Cross-references: UNIPROT:O06427; GB:Z95558; GB:AL123456; NID:g3261781; PIDN:CAB08972.
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv0561c
C:Superfamily: fixC protein

Query Match 68.0%; Score 17; DB 2; Length 408;
Best Local Similarity 28.6%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GXXXXXX 9
Db 18 GSAAAAW 24

RESULT 12
H87193
Probable FAD-linked oxidoreductase ML2276 [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: H87193
R:Coile, S.T.; Eiglmeyer, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: H87193

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-408 <STO>
A;Cross-references: UNIPROT:Q9CBA6; GB:AL450380; NID:g13093912; PIDN:CAC31792.1; GSPDB:G
C;Genetics:
A;Gene: ML2276

Query Match 68.0%; Score 17; DB 2; Length 408;
Best Local Similarity 28.6%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GXXXXXXW 9
Db 18 GSAAATW 24

RESULT 13

C69222
hypothetical protein MTH913 - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Date: 03-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: C69222
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: C69222
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-433 <MTH>
A;Cross-references: UNIPROT:Q26998; GB:AE000867; GB:AE000666; NID:g2622009; PIDN:AAB8541
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH913
A;Start codon: GTG

Query Match 68.0%; Score 17; DB 2; Length 433;
Best Local Similarity 28.6%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GXXXXXXW 9
Db 391 GSASSW 397

RESULT 14

I39591
hemolysin - Aeromonas hydrophila
N;Alternate names: aerolysin
C;Species: Aeromonas hydrophila
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: I39591; I39590; S26573; S26574
R;Hirono, I.; Aoki, T.; Asao, T.; Kozaki, S.
Microb. Pathog. 13, 433-446, 1992
A;Title: Nucleotide sequences and characterization of haemolysin genes from Aeromonas hy
A;Reference number: I39590; MUID:93254202; PMID:1302284
A;Accession: I39591
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-492 <RES>
A;Cross-references: UNIPROT:Q06303; EMBL:X65043; NID:g38816; PIDN:CAA46179.1; PID:g38817
A;Accession: I39590
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-56, 'V', '58-295, 'P', '297-492 <RES2>
A;Cross-references: EMBL:X65044; NID:g38814; PIDN:CAA46180.1; PID:g38815
A;Experimental source: strain 28SA
C;Superfamily: aerolysin

Query Match 68.0%; Score 17; DB 2; Length 492;
Best Local Similarity 28.6%; Pred. No. 4.1e+03;

Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 3 GXXXXXXW 9
Db 91 GSASSTW 97

RESULT 15

T36677
probable secretory protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36677
R;Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, March 1999
A;Reference number: Z21611
A;Accession: T36677
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-523 <SEE>
A;Cross-references: UNIPROT:Q9X921; EMBL:AL035636; PIDN:CAB38493.1; GSPDB:GN00070; SCODE
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCODEB:SCH5.19c

Query Match 68.0%; Score 17; DB 2; Length 523;
Best Local Similarity 28.6%; Pred. No. 4.3e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GXXXXXXW 9
Db 85 GSATTTW 91

Search completed: January 31, 2005, 18:22:34
Job time : 21 secs